

IN THE CLAIMS

1-3. (canceled).

4. (previously presented) A method for sequencing nucleic acids, the method comprising:

- (a) forming an array of immobilised single-stranded template nucleic acid molecules wherein the density of immobilised single-stranded template nucleic acid molecules is 10^6 - 10^9 different template sequences per cm²;
- (b) determining the sequences of the immobilised single-stranded template nucleic acid molecules by synthesising a first complementary copy of each of the template sequences, wherein said synthesising involves repeated cycles of incorporating a single nucleotide into the first complementary copy and detecting incorporation of the single nucleotide into the first complementary copy on the array, thereby performing a first round of sequencing to generate a sequence of the first complementary copy;
- (c) removing the complementary copy of each of the template sequences from the array, thereby regenerating the immobilised single-stranded template molecules on the array;
- (d) performing a second round of sequencing of each of the immobilised single-stranded template nucleic acid molecules regenerated in step (c) by synthesising a second complementary copy of each of the template sequences, wherein said synthesizing involves repeated cycles of incorporating a single nucleotide into the second complementary copy and detecting incorporation of the single nucleotide into the second complementary copy on the array, thereby generating a sequence of the second complementary copy; and
- (e) comparing the sequence of the first complementary copy detected in step (b) to the sequence of the second complementary copy detected in step (d) for each of the immobilized single-stranded template nucleic acid molecules to

confirm sequencing data of each of the immobilized single-stranded template nucleic acid molecules.

5-26. (canceled).

27. (previously presented) The method of claim 4, wherein the immobilised single-stranded template nucleic acid molecules are attached to a double stranded anchor.

28 (previously presented) The method of claim 27, wherein the double stranded anchor comprises a self complementary hairpin.

29 (previously presented) The method of claim 27, wherein the double stranded anchor comprises a recognition site for a restriction endonuclease.

30 (previously presented) The method of claim 4, wherein the 10^6 - 10^9 different template sequences are individually resolvable single molecules.

31 (previously presented) The method of claim 4, wherein the sequencing determination is carried out using cycles of incorporation and detection of fluorescently labeled nucleotides.

32 (previously presented) The method of claim 31, wherein the fluorescently labeled nucleotides are detected using a microscope with total internal reflection based imaging.

33. (previously presented) The method of claim 4, wherein said synthesizing a complementary copy of the template sequences comprises employing a polymerase enzyme to synthesize a complementary sequence one base at a time.

34. (previously presented) The method of claim 4, wherein the comparing the sequence of the first complementary copy to the sequence of the second complementary copy for each of the immobilized single-stranded template nucleic acid molecules reduces random sequencing errors of the template sequences arising from the first round of sequencing.

35. (previously presented) A method for simultaneously sequencing a complete genome comprising a plurality of different nucleic acids, the method comprising:

- (a) forming an array of immobilised single-stranded template nucleic acid molecules wherein the density of immobilised single-stranded template nucleic acid molecules is 10^6 - 10^9 different template sequences per cm^2 ;
- (b) determining the sequences of the immobilised single-stranded template nucleic acid molecules by simultaneously synthesising a first complementary copy of each of the template sequences, wherein said synthesising comprises repeated cycles of single nucleotide incorporation and detection of the single nucleotide incorporated into the first complementary copy on the array, thereby performing a first round of sequencing;
- (c) removing the complementary copy of each of the template sequences from the array, thereby regenerating the immobilised single-stranded template molecules on the array;
- (d) performing a second round of sequencing of each of the immobilised single-stranded template nucleic acid molecules regenerated in step (c) by simultaneously synthesising a second complementary copy of each of the template sequences, wherein said synthesizing involves repeated cycles of single nucleotide incorporation and detection of the single nucleotide incorporated into the second complementary copy on the array; and
- (e) comparing sequences determined for the first complementary copy detected in step (b) and the second complementary copy detected in step (d) of

each immobilized single-stranded template nucleic acid molecule to confirm sequencing data for each immobilized single-stranded template nucleic acid molecule, thereby sequencing the complete genome.

36. (previously presented) A method for sequencing nucleic acids, the method comprising:

- (a) forming an array of immobilised single-stranded template nucleic acid molecules wherein the density of immobilised single-stranded template nucleic acid molecules is 10^6 - 10^9 different template sequences per cm^2 ;
- (b) determining the sequences of the immobilised single-stranded template nucleic acid molecules by simultaneously synthesising a first complementary copy of each of the template sequences, wherein said synthesizing involves repeated cycles of single nucleotide incorporation and detection of the single nucleotide incorporated, thereby performing a first round of sequencing, wherein incorporation and detection are performed on the array;
- (c) removing the complementary copy of each of the template sequences to recover an array of sequenced immobilised single-stranded template nucleic acid molecules;
- (d) performing a second round of sequencing of each of the immobilised single-stranded template nucleic acid molecules on the recovered array of sequenced immobilised single-stranded template nucleic acid molecules by simultaneously synthesising a second complementary copy of each of the template sequences, wherein said synthesizing involves repeated cycles of single nucleotide incorporation and detection of the single nucleotide incorporated, and incorporation and detection are performed on the array; and
- (e) comparing the first round of sequencing detected in step (b) and the second round of sequencing detected in step (d) of each immobilized single-

stranded template nucleic acid molecule to confirm sequencing data for each immobilized single-stranded template nucleic acid molecule.